IN THE SPECIFICATION:

On p. 2, l. 16, delete sis required".

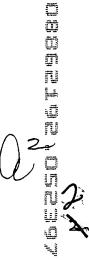
On p. 6, 1. 23, replace the blank with the Division of Biological Sciences for the University of Missouri".

IN THE CLAIMS:

- 1. (Amended) A <u>computer-implemented</u> method for identifying relative binding motifs of peptide-like molecules, comprising the steps of:
 - training [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptide-like molecules, each of known sequence and binding affinity;
 - (b) applying to the ANN <u>input data characterizing</u> at least one <u>test</u> peptide-like molecule, each of known sequence but unknown binding affinity;
 - (c) analyzing each applied test peptide-like molecule using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide-like molecule, and outputting such prediction.

(Amended) A <u>computer-implemented</u> method for identifying relative peptide binding motifs, comprising the steps of:

- (a) training [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (b) applying to the ANN input data characterizing at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (c) analyzing each applied test peptide using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide, and outputting such prediction.



(Amended) The method of claim wherein the set of training peptides include peptides having a binding affinity for [MHC] major histocompatibility complex (MHC) class I molecules.

Y.

(*Reiterated*) The method of claim, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.

025

(*Reiterated*) The method of claim wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

X

(*Reiterated*) The method of claim wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

(Reiterated) The method of claims 1 or wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

- 8. A <u>computer-implemented</u> system for identifying relative binding motifs for peptide-like molecules, comprising:
 - (a) means for training [an] <u>a computer-implemented</u> artificial neural network (ANN) with <u>input data characterizing</u> a set of training peptide-like molecules, each of known sequence and binding affinity;
 - (b) means for applying to the ANN <u>input data characterizing</u> at least one test peptide-like molecule, each of known sequence but unknown binding affinity;
 - (c) means for analyzing each applied test peptide-like molecule using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide-like molecule, and output such prediction.

A <u>computer-implemented</u> system for identifying relative peptide binding motifs, comprising:

- (a) means for training [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (b) means for applying to the ANN <u>input data characterizing</u> at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (c) means for analyzing each applied test peptide using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide, and output such prediction.



(Amended) The system of claim wherein the set of training peptides include peptides having a binding affinity for [MHC] major histocompatibility complex (MHC) class I molecules.

(*Reiterated*) The system of claim N, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b .

(*Reiterated*) The system of claim , wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

(Reiterated) The system of claim 12, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

(Reiterated) The system of claims 8 or $\sqrt{2}$, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

- 15. (Amended) A computer program, residing on a computer-readable medium, for identifying relative binding motifs for peptide-like molecules, comprising instructions for causing a computer to:
 - (a) train [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptide-like molecules, each of known sequence and binding affinity;
 - (b) apply to the ANN <u>input data characterizing</u> at least one test peptide-like molecule, each of known sequence but unknown binding affinity;
 - (c) analyze each applied test peptide-like molecule using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide-like molecule, and output such prediction.

(Amended) A computer program, residing on a computer-readable medium, for identifying relative peptide binding motifs, comprising instructions for causing a computer to:

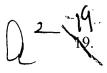
- (a) train [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (b) apply to the ANN input data characterizing at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (c) analyze each applied test peptide using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide, and output such prediction.



(Amended) The computer program of claim K, wherein the set of training peptides having a binding affinity for [MHC] major histocompatiblity complex (MHC) class I molecules.



(*Reiterated*) The computer program of claim 7, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.



(Reiterated) The computer program of claim (4), wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.



(*Reiterated*) The computer program of claim , wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.



(*Reiterated*) The computer program of claims 15 or who, wherein the ANN comprises a multilayer perceptron ANN trained by back-propagation of error.